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Atty. Docket No: 065691/0222

Serial No. 09/853,033

Filed: May 11, 2001

For: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION MEDIATED  
BY MODIFIED CRE-ER

STATEMENT TO SUPPORT FILING AND SUBMISSION IN  
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;


2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and

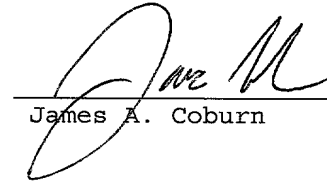
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 09/853,033

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

 06, 2001  
Date

  
James A. Coburn

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09853033-000001



# SEQUENCE LISTING

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[illegible]

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Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser	
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Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu	
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acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg gac	1440
Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp	
465 470 475 480	
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Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr	
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Ala	Asn 290	Leu	Trp	Pro	Ser	Pro 295	Leu	Met	Ile	Lys 300	Arg	Ser	Lys	Lys	Asn
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Ser	Arg	Phe 435	Arg	Met	Met	Asn	Leu 440	Gln	Gly	Glu	Glu	Phe 445	Val	Cys	Leu
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<212> DNA
<213> Artificial sequence

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<222> (1)..(1983)

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gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
           35               40               45

tgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
   50               55               60

ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
   65               70               75               80

cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac
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<211> 1983
<212> DNA
<213> Artificial sequence
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<220>  
<221> CDS  
<222> (1) .. (1983)
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<223> Description of Artificial Sequence: Chimeric sequence  
Homosapiens-Bacteriophage P1

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      1             5             10             15
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gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg  
Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg  
20 25 30

gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt  
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
35 40 45

tgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt  
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
50 55 60

ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg  
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
65 70 75 80

cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac  
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn

85                      90                      95



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100 105 110	
gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt	384
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly	
115 120 125	
gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag	432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln	
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Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn	
145 150 155 160	
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165 170 175	
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Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg	
180 185 190	
atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt	624
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Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile	
260 265 270	
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Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly	
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His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val	
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Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile	
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Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val	
325 330 335	
cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga	1056
Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg	
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Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys	
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Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg	
385 390 395 400	
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Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp	
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Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe	
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Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp	
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Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro	
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465 470 475 480	
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Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr	
485 490 495	
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Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys	
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Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser	
515 520 525	
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Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly
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Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile
				260					265				270		
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly
				275					280				285		
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val
				290					295				300		
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile
				305					310				315		
Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val
				325					330				335		
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg
				340					345				350		
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys
				355					360				365		
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu
				370					375				380		

Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg  
 385 390 395 400  
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp  
 405 410 415  
 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe  
 420 425 430  
 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp  
 435 440 445  
 Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro  
 450 455 460  
 Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly  
 465 470 475 480  
 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr  
 485 490 495  
 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys  
 500 505 510  
 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser  
 515 520 525  
 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu  
 530 535 540  
 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu  
 545 550 555 560  
 Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu  
 565 570 575  
 Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu His Leu Tyr Ser  
 580 585 590  
 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met  
 595 600 605  
 Leu Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser  
 610 615 620  
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser  
 625 630 635 640  
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe  
 645 650 655  
 Pro Ala Thr Val  
 660

&lt;210&gt; 5

&lt;211&gt; 1983

&lt;212&gt; DNA

<213> Artificial sequence

<220>

<221> CDS

<222> (1)..(1983)

<220>

<223> Description of Artificial Sequence: Chimeric sequence  
Homosapiens-Bacteriophage P1

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Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val	
1 5 10 15	
gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg	96
Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg	
20 25 30	
gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt	144
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val	
35 40 45	
tgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt	192
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe	
50 55 60	
ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg	240
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala	
65 70 75 80	
cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac	288
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn	
85 90 95	
atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct	336
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala	
100 105 110	
gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt	384
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly	
115 120 125	
gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag	432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln	
130 135 140	
gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat	480
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn	
145 150 155 160	
ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa	528
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu	
165 170 175	
att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga	576
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg	
180 185 190	

T03080 "E03080" 660

atg	tta	atc	cat	att	ggc	aga	acg	aaa	acg	ctg	gtt	agc	acc	gca	ggt	624
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	
		195					200					205				
gta	gag	aag	gca	ctt	agc	ctg	ggg	gta	act	aaa	ctg	gtc	gag	cga	tgg	672
Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	
		210				215					220					
att	tcc	gtc	tct	ggg	gta	gct	gat	gat	ccg	aat	aac	tac	ctg	ttt	tgc	720
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	
225					230					235					240	
cgg	gtc	aga	aaa	aat	ggg	gtt	gcc	gcg	cca	tct	gcc	acc	agc	cag	cta	768
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	
				245					250					255		
tca	act	cgc	gcc	ctg	gaa	ggg	att	ttt	gaa	gca	act	cat	cga	ttg	att	816
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	
			260					265					270			
tac	ggc	gct	aag	gat	gac	tct	ggg	cag	aga	tac	ctg	gcc	tgg	tct	gga	864
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	
		275					280					285				
cac	agt	gcc	cgt	gtc	gga	gcc	gcg	cga	gat	atg	gcc	cgc	gct	gga	gtt	912
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
		290				295					300					
tca	ata	ccg	gag	atc	atg	caa	gct	ggg	ggc	tgg	acc	aat	gta	aat	att	960
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
305					310					315					320	
gtc	atg	aac	tat	atc	cgt	aac	ctg	gat	agt	gaa	aca	ggg	gca	atg	gtg	1008
Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
				325					330					335		
cgc	ctg	ctg	gaa	gat	ggc	gat	ctc	gag	cca	tct	gct	gga	gac	atg	aga	1056
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	
			340					345					350			
gct	gcc	aac	ctt	tgg	cca	agc	ccg	ctc	atg	atc	aaa	cgc	tct	aag	aag	1104
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	
		355					360					365				
aac	agc	ctg	gcc	ttg	tcc	ctg	acg	gcc	gac	cag	atg	gtc	agt	gcc	ttg	1152
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	
		370				375					380					
ttg	gat	gct	gag	ccc	ccc	ata	ctc	tat	tcc	gag	tat	gat	cct	acc	aga	1200
Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	
385					390					395					400	
ccc	ttc	agt	gaa	gct	tcg	atg	atg									

agg gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca ggc ttt	1296
Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe	
420 425 430	
gtg gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg	1344
Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp	
435 440 445	
cta gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca	1392
Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro	
450 455 460	
gtg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga	1440
Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly	
465 470 475 480	
aaa tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca	1488
Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr	
485 490 495	
tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc	1536
Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys	
500 505 510	
ctc aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc	1584
Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser	
515 520 525	
agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg	1632
Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu	
530 535 540	
gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg	1680
Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu	
545 550 555 560	
acc ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc	1728
Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu	
565 570 575	
tcc cac atc agg cac atg agt aac aaa ggc atg gag cat ctg tac agc	1776
Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser	
580 585 590	
atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag gcg	1824
Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala	
595 600 605	
gcg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc	1872
Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser	
610 615 620	
gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca	1920
Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser	
625 630 635 640	



cct gcc aca gct tga 1983  
Pro Ala Thr Ala  
660

<220>  
<223> Description of Artificial Sequence: Chimeric sequence  
Homosapiens-Bacteriophage P1

<400>	6														
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Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg
			20					25					30		
Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val
		35					40					45			
Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe
	50					55					60				
Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala
65					70					75					80
Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn
				85					90					95	
Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala
			100					105					110		
Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly
		115					120					125			
Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln
	130					135					140				
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn
145					150					155					160
Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu
				165					170					175	
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg
			180					185					190		
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly
		195					200					205			

Val 210	Glu	Lys	Ala	Leu	Ser	Leu 215	Gly	Val	Thr	Lys	Leu 220	Val	Glu	Arg	Trp
Ile 225	Ser	Val	Ser	Gly	Val 230	Ala	Asp	Asp	Pro	Asn 235	Asn	Tyr	Leu	Phe	Cys 240
Arg	Val	Arg	Lys	Asn 245	Gly	Val	Ala	Ala	Pro 250	Ser	Ala	Thr	Ser	Gln 255	Leu
Ser	Thr	Arg	Ala 260	Leu	Glu	Gly	Ile	Phe 265	Glu	Ala	Thr	His	Arg 270	Leu	Ile
Tyr	Gly	Ala 275	Lys	Asp	Asp	Ser	Gly 280	Gln	Arg	Tyr	Leu 285	Ala	Trp	Ser	Gly
His 290	Ser	Ala	Arg	Val	Gly 295	Ala	Ala	Arg	Asp	Met 300	Ala	Arg	Ala	Gly	Val
Ser 305	Ile	Pro	Glu	Ile 310	Met	Gln	Ala	Gly	Gly 315	Trp	Thr	Asn	Val	Asn 320	Ile
Val	Met	Asn	Tyr	Ile 325	Arg	Asn	Leu	Asp	Ser 330	Glu	Thr	Gly	Ala	Met 335	Val
Arg	Leu	Leu	Glu 340	Asp	Gly	Asp	Leu	Glu 345	Pro	Ser	Ala	Gly	Asp 350	Met	Arg
Ala	Ala 355	Asn	Leu	Trp	Pro	Ser 360	Pro	Leu	Met	Ile	Lys 365	Arg	Ser	Lys	Lys
Asn 370	Ser	Leu	Ala	Leu	Ser 375	Leu	Thr	Ala	Asp	Gln 380	Met	Val	Ser	Ala	Leu
Leu 385	Asp	Ala	Glu	Pro 390	Pro	Ile	Leu	Tyr	Ser 395	Glu	Tyr	Asp	Pro	Thr	Arg 400
Pro	Phe	Ser	Glu 405	Ala	Ser	Met	Met	Gly 410	Leu	Leu	Thr	Asn	Leu 415	Ala	Asp
Arg	Glu	Leu	Val 420	His	Met	Ile	Asn 425	Trp	Ala	Lys	Arg	Val 430	Pro	Gly	Phe
Val	Asp 435	Leu	Thr	Leu	His	Asp 440	Gln	Val	His	Leu	Leu 445	Glu	Cys	Ala	Trp
Leu 450	Glu	Ile	Leu	Met	Ile 455	Gly	Leu	Val	Trp	Arg 460	Ser	Met	Glu	His	Pro
Val 465	Lys	Leu	Leu	Phe 470	Ala	Pro	Asn	Leu	Leu 475	Leu	Asp	Arg	Asn	Gln	Gly 480
Lys	Cys	Val	Glu 485	Gly	Met	Val	Glu	Ile 490	Phe	Asp	Met	Leu	Leu 495	Ala	Thr
Ser	Ser	Arg	Phe 500	Arg	Met	Met	Asn 505	Leu	Gln	Gly	Glu 510	Glu	Phe	Val	Cys

Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser  
 515 520 525  
 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu  
 530 535 540  
 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu  
 545 550 555 560  
 Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu  
 565 570 575  
 Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser  
 580 585 590  
 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala  
 595 600 605  
 Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser  
 610 615 620  
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser  
 625 630 635 640  
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe  
 645 650 655  
 Pro Ala Thr Ala  
 660

<210> 7

<211> 1983

<212> DNA

<213> Artificial sequence

<220>

<221> CDS

<222> (1)..(1983)

<220>

<223> Description of Artificial Sequence: Chimeric sequence  
 Homosapiens-Bacteriophage P1

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gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg 96  
 Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg  
 20 25 30

gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144  
 Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
 35 40 45

tgc Cys	cgg Arg	tcg Ser	tgg Trp	gcg Ala	gca Ala	tgg Trp	tgc Cys	aag Lys	ttg Leu	aat Asn	aac Asn	cgg Arg	aaa Lys	tgg Trp	ttt Phe	192
505560																
ccc Pro	gca Ala	gaa Glu	cct Pro	gaa Glu	gat Asp	gtt Val	cgc Arg	gat Asp	tat Tyr	ctt Leu	cta Leu	tat Tyr	ctt Leu	cag Gln	gcg Ala	240
65707580																
cgc Arg	ggg Gly	ctg Leu	gca Ala	gta Val	aaa Lys	act Thr	atc Ile	cag Gln	caa Gln	cat His	ttg Leu	ggc Gly	cag Gln	cta Leu	aac Asn	288
859095																
atg Met	ctt Leu	cat His	cgt Arg	cgg Arg	tcc Ser	ggg Gly	ctg Leu	cca Pro	cga Arg	cca Pro	agt Ser	gac Asp	agc Ser	aat Asn	gct Ala	336
100105110																
gtt Val	tca Ser	ctg Leu	gtt Val	atg Met	cgg Arg	cgg Arg	atc Ile	cga Arg	aaa Lys	gaa Glu	aac Asn	gtt Val	gat Asp	gcc Ala	ggg Gly	384
115120125																
gaa Glu	cgt Arg	gca Ala	aaa Lys	cag Gln	gct Ala	cta Leu	gcg Ala	ttc Phe	gaa Glu	cgc Arg	act Thr	gat Asp	ttc Phe	gac Asp	cag Gln	432
130135140																
gtt Val	cgt Arg	tca Ser	ctc Leu	atg Met	gaa Glu	aat Asn	agc Ser	gat Asp	cgc Arg	tgc Cys	cag Gln	gat Asp	ata Ile	cgt Arg	aat Asn	480
145150155160																
ctg Leu	gca Ala	ttt Phe	ctg Leu	ggg Gly	att Ile	gct Ala	tat Tyr	aac Asn	acc Thr	ctg Leu	tta Leu	cgt Arg	ata Ile	gcc Ala	gaa Glu	528
165170175																
att Ile	gcc Ala	agg Arg	atc Ile	agg Arg	gtt Val	aaa Lys	gat Asp	atc Ile	tca Ser	cgt Arg	act Thr	gac Asp	ggg Gly	ggg Gly	aga Arg	576
180185190																
atg Met	tta Leu	atc Ile	cat His	att Ile	ggc Gly	aga Arg	acg Thr	aaa Lys	acg Thr	ctg Leu	gtt Val	agc Ser	acc Thr	gca Ala	ggg Gly	624
195200205																
gta Val	gag Glu	aag Lys	gca Ala	ctt Leu	agc Ser	ctg Leu	ggg Gly	gta Val	act Thr	aaa Lys	ctg Leu	gtc Val	gag Glu	cga Arg	tgg Trp	672
210215220																
att Ile	tcc Ser	gtc Val	tct Ser	ggg Gly	gta Val	gct Ala	gat Asp	gat Asp	ccg Pro	aat Asn	aac Asn	tac Tyr	ctg Leu	ttt Phe	tgc Cys	720
225230235240																
cgg Arg	gtc Val	aga Arg	aaa Lys	aat Asn	ggg Gly	gtt Val	gcc Ala	gcg Ala	cca Pro	tct Ser	gcc Ala	acc Thr	agc Ser	cag Gln	cta Leu	768
245250255																
tca Ser	act Thr	cgc Arg	gcc Ala	ctg Leu	gaa Glu	ggg Gly	att Ile	ttt Phe	gaa Glu	gca Ala	act Thr	cat His	cga Arg	ttg Leu	att Ile	816
260265270																

tac Tyr	ggc Gly	gct Ala 275	aag Lys	gat Asp	gac Asp	tct Ser	ggt Gly 280	cag Gln	aga Arg	tac Tyr	ctg Leu	gcc Ala 285	tgg Trp	tct Ser	gga Gly	864
cac His	agt Ser 290	gcc Ala	cgt Arg	gtc Val	gga Gly 295	gcc Ala	gcg Ala	cga Arg	gat Asp	atg Met 300	gcc Ala	cgc Arg	gct Ala	gga Gly	ggt Val	912
tca Ser 305	ata Ile	ccg Pro	gag Glu	atc Ile 310	atg Met	caa Gln	gct Ala	ggt Gly	ggc Gly	tgg Trp 315	acc Thr	aat Asn	gta Val	aat Asn	att Ile 320	960
gtc Val	atg Met	aac Asn	tat Tyr	atc Ile 325	cgt Arg	aac Asn	ctg Leu	gat Asp 330	agt Ser	gaa Glu	aca Thr	ggg Gly	gca Ala	atg Met 335	gtg Val	1008
cgc Arg	ctg Leu	ctg Leu	gaa Glu 340	gat Asp	ggc Gly	gat Asp	ctc Leu	gag Glu 345	cca Pro	tct Ser	gct Ala	gga Gly	gac Asp 350	atg Met	aga Arg	1056
gct Ala	gcc Ala 355	aac Asn	ctt Leu	tgg Trp	cca Pro	agc Ser 360	ccg Pro	ctc Leu	atg Met	atc Ile	aaa Lys 365	cgc Arg	tct Ser	aag Lys	aag Lys	1104
aac Asn 370	agc Ser	ctg Leu	gcc Ala	ttg Leu	tcc Ser 375	ctg Leu	acg Thr	gcc Ala	gac Asp	cag Gln 380	atg Met	gtc Val	agt Ser	gcc Ala	ttg Leu	1152
ttg Leu 385	gat Asp	gct Ala	gag Glu	ccc Pro 390	ccc Pro	ata Ile	ctc Leu	tat Tyr	tcc Ser 395	gag Glu	tat Tyr	gat Asp	cct Pro	acc Thr	aga Arg 400	1200
ccc Pro	ttc Phe	agt Ser	gaa Glu 405	gct Ala	tcg Ser	atg Met	atg Met	ggc Gly 410	tta Leu	ctg Leu	acc Thr	aac Asn	ctg Leu	gca Ala 415	gac Asp	1248
agg Arg	gag Glu	ctg Leu 420	gtt Val	cac His	atg Met	atc Ile	aac Asn 425	tgg Trp	gcg Ala	aag Lys	agg Arg	gtg Val 430	cca Pro	ggc Gly	ttt Phe	1296
gtg Val	gat Asp 435	ttg Leu	acc Thr	ctc Leu	cat His	gat Asp 440	cag Gln	gtc Val	cac His	ctt Leu	cta Leu	gaa Glu 445	tgt Cys	gcc Ala	tgg Trp	1344
cta Leu 450	gag Glu	atc Ile	ctg Leu	atg Met	att Ile 455	ggt Gly	ctc Leu	gtc Val	tgg Trp	cgc Arg 460	tcc Met	atg Met	gag Glu	cac His	cca Pro	1392
ggg Gly 465	aag Lys	cta Leu	ctg Leu	ttt Phe 470	gct Ala	cct Pro	aac Asn	ttg Leu	ctc Leu	ttg Leu 475	gac Asp	agg Arg	aac Asn	cag Gln	gga Gly 480	1440
aaa Lys	tgt Cys	gta Val	gag Glu 485	ggc Gly	atg Met	gtg Val	gag Glu	atc Ile 490	ttc Phe	gac Asp	atg Met	ctg Leu	ctg Leu	gct Ala 495	aca Thr	1488

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 Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
 35 40 45  
 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
 50 55 60  
 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
 65 70 75 80  
 Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
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 Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
 100 105 110  
 Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
 115 120 125  
 Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln  
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 Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
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 Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
 165 170 175  
 Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg  
 180 185 190  
 Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
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 Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp  
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 Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
 225 230 235 240  
 Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu  
 245 250 255  
 Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
 260 265 270  
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly  
 275 280 285  
 His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
 290 295 300  
 Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile  
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T03080" E0000000

Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
				325					330					335		
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	
				340					345					350		
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	
				355					360					365		
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	
				370					375					380		
Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	
				385					390					395		
Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	
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Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	
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Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	
				435					440					445		
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro	
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Gly	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly	
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Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	
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Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys	
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Leu	Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val	Tyr	Thr	Phe	Leu	Ser	
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Ser	Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His	Ile	His	Arg	Val	Leu	
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Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met	Ala	Lys	Ala	Gly	Leu	
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Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu	
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Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser	
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Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Leu	Tyr	Asp	Leu	Leu	Leu	Glu	Ala	
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Ala	Asp	Ala	His	Arg	Leu	His	Ala	Pro	Thr	Ser	Arg	Gly	Gly	Ala	Ser	
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37